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## RAW SEQUENCE LISTING

DATE: 07/02/2001

PATENT APPLICATION: US/09/754,947

TIME: 16:41:09

Input Set : A:\-33-1.app

Output Set: N:\CRF3\07022001\I754947.raw

ENTERED

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3 <110> APPLICANT: Lee, Bruce Andrew
4     Flores, Becky Mar
5     Valkirs, Gunars Edwin
6     Biosite Diagnostics, Inc.
8 <120> TITLE OF INVENTION: Assays for Detection of Bacillus Anthracis
10 <130> FILE REFERENCE: 014907-003310US
12 <140> CURRENT APPLICATION NUMBER: US 09/754,947
13 <141> CURRENT FILING DATE: 2001-01-04
15 <150> PRIOR APPLICATION NUMBER: US 60/174,901
16 <151> PRIOR FILING DATE: 2000-01-06
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 785
24 <212> TYPE: PRT
25 <213> ORGANISM: Bacillus anthracis
27 <220> FEATURE:
28 <223> OTHER INFORMATION: surface array protein (SAP)
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31 Ala Gly Lys Thr Phe Pro Asp Val Pro Ala Asp His Trp Gly Ile Asp
32   1             5             10             15
34 Ser Ile Asn Tyr Leu Val Glu Lys Gly Ala Val Lys Gly Asn Asp Lys
35           20           25           30
37 Gly Met Phe Glu Pro Gly Lys Glu Leu Thr Arg Ala Glu Ala Ala Thr
38         35         40         45
40 Met Met Ala Gln Ile Leu Asn Leu Pro Ile Asp Lys Asp Ala Lys Pro
41       50       55       60
43 Ser Phe Ala Asp Ser Gln Gly Gln Trp Tyr Thr Pro Phe Ile Ala Ala
44   65           70           75           80
46 Val Glu Lys Ala Gly Val Ile Lys Gly Thr Gly Asn Gly Phe Glu Pro
47         85         90         95
49 Asn Gly Lys Ile Asp Arg Val Ser Met Ala Ser Leu Leu Val Glu Ala
50       100       105       110
52 Tyr Lys Leu Asp Thr Lys Val Asn Gly Thr Pro Ala Thr Lys Phe Lys
53     115     120     125
55 Asp Leu Glu Thr Leu Asn Trp Gly Lys Glu Lys Ala Asn Ile Leu Val
56   130   135   140
58 Glu Leu Gly Ile Ser Val Gly Thr Gly Asp Gln Trp Glu Pro Lys Lys
59 145   150   155   160
61 Thr Val Thr Lys Ala Glu Ala Ala Gln Phe Ile Ala Lys Thr Asp Lys
62       165       170       175
64 Gln Phe Gly Thr Glu Ala Ala Lys Val Glu Ser Ala Lys Ala Val Thr
65     180     185     190
67 Thr Gln Lys Val Glu Val Lys Phe Ser Lys Ala Val Glu Lys Leu Thr
68   195   200   205
70 Lys Glu Asp Ile Lys Val Thr Asn Lys Ala Asn Asn Asp Lys Val Leu
71   210   215   220

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73 Val Lys Glu Val Thr Leu Ser Glu Asp Lys Arg Ser Ala Thr Val Glu
74 225                230                235                240
76 Leu Tyr Ser Asn Leu Ala Ala Lys Gln Thr Tyr Thr Val Asp Val Asn
77                245                250                255
79 Lys Val Gly Lys Thr Glu Val Ala Val Gly Ser Leu Glu Ala Lys Thr
80                260                265                270
82 Ile Glu Met Ala Asp Gln Thr Val Val Ala Asp Glu Pro Thr Ala Leu
83                275                280                285
85 Gln Phe Thr Val Lys Asp Glu Asn Gly Thr Glu Val Val Ser Pro Glu
86                290                295                300
88 Gly Ile Glu Phe Val Thr Pro Ala Ala Glu Lys Ile Asn Ala Lys Gly
89 305                310                315                320
91 Glu Ile Thr Leu Ala Lys Gly Thr Ser Thr Thr Val Lys Ala Val Tyr
92                325                330                335
94 Lys Lys Asp Gly Lys Val Val Ala Glu Ser Lys Glu Val Lys Val Ser
95                340                345                350
97 Ala Glu Gly Ala Ala Val Ala Ser Ile Ser Asn Trp Thr Val Ala Glu
98                355                360                365
100 Gln Asn Lys Ala Asp Phe Thr Ser Lys Asp Phe Lys Gln Asn Asn Lys
101                370                375                380
103 Val Tyr Glu Gly Asp Asn Ala Tyr Val Gln Val Glu Leu Lys Asp Gln
104 385                390                395                400
106 Phe Asn Ala Val Thr Thr Gly Lys Val Glu Tyr Glu Ser Leu Asn Thr
107                405                410                415
109 Glu Val Ala Val Val Asp Lys Ala Thr Gly Lys Val Thr Val Leu Ser
110                420                425                430
112 Ala Gly Lys Ala Pro Val Lys Val Thr Val Lys Asp Ser Lys Gly Lys
113                435                440                445
115 Ala Leu Val Ser His Thr Val Glu Ile Glu Ala Phe Ala Gln Lys Ala
116                450                455                460
118 Met Lys Asp Ile Lys Leu Glu Lys Thr Asn Val Ala Leu Ser Thr Lys
119 465                470                475                480
121 Asp Val Thr Asp Leu Lys Val Lys Ala Pro Val Leu Asp Gln Tyr Gly
122                485                490                495
124 Lys Glu Phe Thr Ala Pro Val Thr Val Lys Val Leu Asp Lys Asp Gly
125                500                505                510
127 Lys Glu Leu Lys Glu Gln Lys Leu Glu Ala Lys Tyr Val Asn Arg Glu
128                515                520                525
130 Leu Val Leu Asn Ala Ala Gly Gln Glu Ala Gly Asn Tyr Thr Val Val
131                530                535                540
133 Leu Thr Ala Lys Ser Gly Glu Lys Glu Ala Lys Ala Thr Leu Ala Leu
134 545                550                555                560
136 Glu Leu Lys Ala Pro Gly Ala Phe Ser Lys Phe Glu Val Arg Gly Leu
137                565                570                575
139 Asp Thr Glu Leu Asp Lys Tyr Val Thr Glu Glu Asn Gln Lys Asn Ala
140                580                585                590
142 Met Thr Val Ser Val Leu Pro Val Asp Ala Asn Gly Leu Val Leu Lys
143                595                600                605
145 Gly Ala Glu Ala Ala Glu Leu Lys Val Thr Thr Thr Asn Lys Glu Gly

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146      610      615      620
148 Lys Glu Val Asp Ala Thr Asp Ala Gln Val Thr Val Gln Asn Asn Ser
149 625      630      635      640
151 Val Ile Thr Val Gly Gln Gly Ala Lys Ala Gly Glu Thr Tyr Lys Val
152      645      650      655
154 Thr Val Val Leu Asp Gly Lys Leu Ile Thr Thr His Ser Phe Lys Val
155      660      665      670
157 Val Asp Thr Ala Pro Thr Ala Lys Gly Leu Ala Val Glu Phe Thr Ser
158      675      680      685
160 Thr Ser Leu Lys Glu Val Ala Pro Asn Ala Asp Leu Lys Ala Ala Leu
161      690      695      700
163 Leu Asn Ile Leu Ser Val Asp Gly Val Pro Ala Thr Thr Ala Lys Ala
164 705      710      715      720
166 Thr Ala Ser Asn Val Glu Phe Val Ser Ala Asp Thr Asn Val Val Ala
167      725      730      735
169 Glu Asn Gly Thr Val Gly Ala Lys Gly Ala Thr Ser Ile Tyr Val Lys
170      740      745      750
172 Asn Leu Thr Val Val Lys Asp Gly Lys Glu Gln Lys Val Glu Phe Asp
173      755      760      765
175 Lys Ala Val Gln Val Ala Val Ser Ile Lys Glu Ala Lys Pro Ala Thr
176      770      775      780
178 Lys
179 785
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 2370
184 <212> TYPE: DNA
185 <213> ORGANISM: Bacillus anthracis
187 <220> FEATURE:
188 <223> OTHER INFORMATION: surface array protein (SAP)
190 <400> SEQUENCE: 2
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192 gaaaaaggcg cagttaaagg taacgacaaa ggaatgttcg agcctggaaa agaattaact 120
193 cgtgcagaag cagctacaat gatggctcaa atcttaact taccaatcga taaagatgct 180
194 aaaccatctt tcgctgactc tcaaggccaa tggtagactc cattcatcgc agctgtagaa 240
195 aaagctggcg ttattaaagg tacaggaaac ggctttgagc caaacggaaa aatcgaccgc 300
196 gtttctatgg catctcttct tgtagaagct tacaaattag atactaaagt aaacggtact 360
197 ccagcaacta aattcaaaga tttagaaaca ttaaactggg gtaaagaaaa agctaacatc 420
198 ttagttgaat taggaatctc tgttggtact ggtgatcaat gggagcctaa gaaaactgta 480
199 actaaagcag aagctgctca attcattgct aagactgaca agcagttcgg tacagaagca 540
200 gcaaaagttg aatctgcaaa agctgttaca actcaaaaag tagaagttaa attcagcaaa 600
201 gctgttgaaa aattaactaa agaagatatc aaagtaacta acaaagctaa caacgataaa 660
202 gtactagtta aagaggtaac tttatcagaa gataaaagat ctgctacagt tgaattatat 720
203 agtaacttag cagctaaaca aacttacact gtagatgtaa acaaagttgg taaaacagaa 780
204 gtagctgtag gttctttaga agcaaaaaca atcgaaatgg ctgaccaaac agttgtagct 840
205 gatgagccaa cagcattaca attcacagtt aaagatgaaa acggtactga agttgtttca 900
206 ccagagggta ttgaatttgt aacgccagct gcagaaaaaa ttaatgcaaa aggtgaaatc 960
207 acttttagcaa aaggtaactt aactactgta aaagctgttt ataaaaaaga cggtaaagta 1020
208 gtagctgaaa gtaaagaagt aaaagtttct gctgaagggt ctgcagtagc ttcaatctct 1080
209 aactggacag ttgcagaaca aaataaagct gactttactt ctaaagattt caaacaaaac 1140

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210 aataaagttt acgaaggcga caacgcttac gttcaagtag aattgaaaga tcaatttaac 1200
211 gcagtaacaa ctggaaaagt tgaatatgag tcgttaaaca cagaagttgc tgtagtagat 1260
212 aaagctactg gtaaagtaac tgtattatct gcaggaaaag caccagtaaa agtaactgta 1320
213 aaagattcaa aaggtaaagc acttgtttca cacacagttg aaattgaagc tttcgctcaa 1380
214 aaagcaatga aagacattaa attagaaaaa actaacgtag cgctttctac aaaagatgta 1440
215 acagatttaa agtaaaaagc tccagtacta gatcaatacg gtaaagagtt tacagctcct 1500
216 gtaacagtga aagtacttga taaagatggg aaagaattaa aagaacaaaa attagaagct 1560
217 aaatatgtga acagagaatt agttctgaat gcagcaggtc aagaagctgg taattataca 1620
218 gttgtattaa ctgcaaaatc tggtgaaaaa gaagcaaaag ctacattagc tctagaatta 1680
219 aaagctccag gtgcattctc taaatttgaa gttcgtgggt tagacacaga attagataaa 1740
220 tatgttactg aggaaaacca aaagaatgca atgactgttt cagttcttcc tgtagatgca 1800
221 aatggattag tattaanaag tgcagaagca gctgaactaa aagtaacaac aacaaacaaa 1860
222 gaaggtaaaag aagtagacgc aactgatgca caagttactg tacaaaataa cagtgttaatt 1920
223 actgttggtc aagggtgcaa agctggtgag acttataaag taacagttgt actagatggg 1980
224 aaattaatca caactcattc attcaaagtt gttgatacag caccaactgc taaaggatta 2040
225 gcagtagaat ttacaagcac atctcttaaa gaagtagctc caaatgctga tttaaaagct 2100
226 gcacttttaa atatcttata tgttgatggg gtacctgcga ctacagcaaa agcaacagct 2160
227 tctaattgtag aatttgtttc tgctgacaca aatgttgtag ctgaaaatgg tacagttggg 2220
228 gcaaaagggtg caacatctat ctatgtgaaa aacctgacag ttgtaaaaga tggaaaagag 2280
229 caaaaagtag aatttgataa agctgtacaa gttgcagttt ctattaaaga agcaaacct 2340
230 gcaacaaaac atcaccatca ccatcactaa 2370
233 <210> SEQ ID NO: 3
234 <211> LENGTH: 44
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence:5' PCR primer
241 <400> SEQUENCE: 3
242 tcgctgccca accagccatg gccgcaggta aaacattccc agac 44
245 <210> SEQ ID NO: 4
246 <211> LENGTH: 89
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Description of Artificial Sequence:3' PCR primer
253 <400> SEQUENCE: 4
254 gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atgggtgatgg 60
255 tgatgttttg ttgcaggttt tgcttcttt 89
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 201
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence:flexible linker
266 <220> FEATURE:
267 <221> NAME/KEY: MOD_RES
268 <222> LOCATION: (1)..(97)
269 <223> OTHER INFORMATION: Gly at positions 1-97 may be present or absent
271 <220> FEATURE:

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272 <221> NAME/KEY: MOD\_RES  
 273 <222> LOCATION: (105)..(201)  
 274 <223> OTHER INFORMATION: Gly at positions 105-201 may be present or absent  
 276 <400> SEQUENCE: 5  
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 278 1 5 10 15  
 280 Gly  
 281 20 25 30  
 283 Gly  
 284 35 40 45  
 286 Gly  
 287 50 55 60  
 289 Gly  
 290 65 70 75 80  
 292 Gly  
 293 85 90 95  
 295 Gly Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 296 100 105 110  
 298 Gly  
 299 115 120 125  
 301 Gly  
 302 130 135 140  
 304 Gly  
 305 145 150 155 160  
 307 Gly  
 308 165 170 175  
 310 Gly  
 311 180 185 190  
 313 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 314 195 200

VERIFICATION SUMMARY

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